

SEQUENCE LISTING

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<120> MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACTOR-1 BY THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN

<130> 3743/49008

<150> US 60/223,480

<151> 2000-08-07

<160> 7

<170> PatentIn version 3.0

<210> 1

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(639)

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Glu Ala Gly Val Glu Glu Tyr Gly Pro Glu Glu Asp Gly Gly Glu Glu	
20 25 30	
tgg ggc gcc gag gag tcc ggc ccg gaa gag tcc ggc ccg gag gaa ctg	144
Ser Gly Ala Glu Glu Ser Gly Pro Glu Glu Ser Gly Pro Glu Glu Leu	
35 40 45	
ggc gcc gag gag gag atg gag gcc ggg ccg ccg ccg ccc gtg ctg cgc	192
Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg	
50 55 60	

tog gtc aac tog cgc gag ccc tcc cag gtc atc ttc tgc aat cgc agt Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg Ser 65 70 75 80	240
cgc cgc gtc gtc ctg ccc gta tgg etc aac ttc gac ggc gag ccg cag Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln 85 90 95	288
ccc tac cca acg ctg ccg cct ggc acg ggc cgc cgc atc cac agc tac Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr 100 105 110	336
cga ggt cac ctt tgg ctc ttc aga gat gca ggg aca cac gat ggg ctt Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu 115 120 125	384
ctg gtt aac caa act gaa tta ttt gtg cca tct ctc aat gtt gac gga Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly 130 135 140	432
cag cct att ttt gcc aat atc aca ctg cca gtg tat act ctg aaa gag Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys Glu 145 150 155 160	480
cga tgc ctc cag gtt gtc cgg agc cta gtc aag cct gag aat tac agg Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg 165 170 175	528
aga ctg gac atc gtc agg tgc ctc tac gaa gat ctg gaa gac cac cca Arg Leu Asp Ile Val Arg Ser Leu Tyr Asp Glu Asp Leu Glu His Pro 180 185 190	576
aat gtg cag aaa gac ctg gag cgg ctg aca cag gag cgc att gca cat Asn Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu Arg Ile Ala His 195 200 205	624
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<212> PRT

<213> Homo sapiens

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35 40 45

Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg
50 55 60

Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg Ser
65 70 75 80

Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln
85 90 95

Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr
100 105 110

Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu
115 120 125

Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly
130 135 140

Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys Glu
145 150 155 160

Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg
165 170 175

Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp His Pro
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 Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
 20 25 30
 gaa tct gaa gtt ttt tat gag ctt gct cat cag ttg cca ctt cca cat 144
 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
 35 40 45
 aat gtg agt tcg cat ctt gat aag gcc tct gtg atg agg ctt acc atc 192
 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
 50 55 60
 agc tat ttg cgt gtg agg aaa ctt ctg gat gct ggt gat ttg gat att 240
 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
 65 70 75 80
 gaa gat gac atg aaa gca cag atg aat tgc ttt tat ttg aaa gcc ttg 288
 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
 85 90 95
 gat ggt ttt gtt atg gtt ctc aca gat gat ggt gac atg att tac att 336
 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
 100 105 110
 tct gat aat gtg aac aaa tac atg gga tta act cag ttt gaa cta act 384
 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
 115 120 125
 gga cac agt gtg ttt gat ttt act cat cca tgt gac cat gag gaa atg 432
 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
 130 135 140
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 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
 145 150 155 160
 caa aac aca cag cga agc ttt ttt ctc aga atg aag tgt acc cta act 528
 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
 165 170 175
 agc cga gga aga act atg aac ata aag tct gca aca tgg aag gta ttg 576
 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
 180 185 190
 cac tgc aca ggc cac att cac gta tat gat acc aac agt aac caa cct 624
 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
 195 200 205
 cag tgt ggg tat aag aaa cca cct atg acc tgc ttg gtg ctg att tgt 672
 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
 210 215 220
 gaa ccc att cct cac cca tca aat att gaa att cct tta gat agc aag 720
 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
 225 230 235 240
 act ttc ctc agt cga cac agc ctg gat atg aaa ttt tct tat tgt gat 768
 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp

Page 5

Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu	
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cct aat agt ccc agt gaa tat tgt ttt tat gtg gat agt gat atg gtc	1584
Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val	
515 520 525	
aat gaa ttc aag ttg gaa ttg gta gaa aaa ctt ttt gct gaa gac aca	1632
Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr	
530 535 540	
gaa gca aag aac cca ttt tct act cag gac aca gat tta gac ttg gag	1680
Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu	
545 550 555	
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Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Phe Gln Leu Arg Ser	
565 570 575	
ttc gat cag ttg tca cca tta gaa agc agt tcc gca agc cct gaa agc	1776
Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser	
580 585 590	
gca agt cct caa agc aca gtt aca gta ttc cag cag act caa ata caa	1824
Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln	
595 600 605	
gaa cct act gct aat gcc acc act acc act gcc acc act gat gaa tta	1872
Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu	
610 615 620	
aaa aca gtg aca aaa gac cgt atg gaa gac att aaa ata ttg att gca	1920
Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala	
625 630 635	
tct cca tct cct acc cac ata cat aaa gaa act act agt gcc aca tca	1968
Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser	
645 650 655	
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Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala	
660 665 670	
gga aaa gga gtc ata gaa cag aca gaa aaa tct cat cca aga agc cct	2064
Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro	
675 680 685	
aac gtg tta tct gtc gct ttg agt caa aga act aca gtt cct gag gaa	2112
Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu	
690 695 700	
gaa cta aat cca aag ata cta gct ttg cag aat gct cag aga aag cga	2160
Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg	
705 710 715	
aaa atg gaa cat gat ggt tca ctt ttt caa gca gta gga att gga aca	2208
Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr	
725 730 735	
tta tta cag cag cca gac gat cat gca gct act aca tca ctt tct tgg	2256
Leu Leu Gln Gln Pro Asp His Ala Ala Thr Thr Ser Leu Ser Trp	
740 745 750	

aaa cgt gta aaa gga tgc aaa tct agt gaa cag aat gga atg gag caa 2304
Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln
755 760 765

aag aca att att tta ata ccc tct gat tta gca tgt aga ctg ctg ggg 2352
Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly
770 775 780

caa tca atg gat gaa agt gga tta cca cag ctg acc agt tat gat tgt 2400
Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys
785 790 795 800

gaa gtt aat gct cct ata caa ggc agc aga aac cta ctg cag ggt gaa 2448
Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu
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gaa tta ctc aga gct ttg gat caa gtt aac tga 2481
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<212> PRT

<213> Homo sapiens

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35 40 45

Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
50 55 60

Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
65 70 75 80

Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
85 90 95

Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
100 105 110

Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
115 120 125

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Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
130 135 140

Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
145 150 155 160

Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
165 170 175

Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
180 185 190

His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
195 200 205

Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
210 215 220

Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
225 230 235 240

Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
245 250 255

Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly
260 265 270

Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr
275 280 285

Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln
290 295 300

Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
305 310 315 320

Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val
325 330 335

Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe
340 345 350

Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp
355 360 365

Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser
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645 650 655

Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala
660 665 670

Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro
675 680 685

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690 695 700

Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg
705 710 715 720

Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr
725 730 735

Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp
740 745 750

Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln
755 760 765

Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly
770 775 780

Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys
785 790 795 800

Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu
805 810 815

Glu Leu Leu Arg Ala Leu Asp Gln Val Asn
820 825

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<212> PRT

<213> Homo sapiens

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Pro Tyr Ile Pro Met Asp Asp Phe Gln Leu Arg Ser Phe Asp Gln
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Leu Ser Pro Leu Glu Ser
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<213> Artificial

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<223> Description of Artificial Sequence: Oligonucleotides containing
HindIII and Bst98I restriction site

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<212> DNA

<213> Artificial

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<223> Description of Artificial Sequence: Oligonucleotides containing
HindIII and Bst98I restriction site

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